



<110> BECQUART, JEROME

<120> ALBUMIN DERIVATIVES WITH THERAPEUTIC FUNCTIONS

<130> 06832.1429-03

<140> 10/073,118

<141> 2002-02-12

<150> 09/551,635

<151> 2000-04-18

<150> 09/004,319

<151> 1998-01-08

<150> 08/479,146

<151> 1995-06-07

<150> 08/295,078

<151> 1994-08-26

<150> 08/121,236

<151> 1993-09-13

<150> 07/955,243

<151> 1992-10-01

<150> 07/561,879

<151> 1990-08-02

<150> FR 89 10480

<151> 1989-08-03

<160> 41

<170> PatentIn Ver. 2.1

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<211> 13

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restriction site

<220>

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<222> (5)..(9)

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<400> 1

ggccnnnnng gcc

<210> 2  
 <211> 31  
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 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligodeoxynucleotide

<400> 2  
 atctaaggaa atacaagctt atgaagtggg t

31

<210> 3  
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 oligonucleotide

<400> 3  
 taaaaacaaa agatccccaa gcttggggat ctcccatgtc tctact

46

<210> 4  
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<400> 4  
 gatccgtcga cg

12

<210> 5  
 <211> 28  
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<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide

<400> 5  
 aagctttaca acaaataaa aaacaatg

28

<210> 6  
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<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide

<400> 6  
ttacattatt aatttaaaaa tggattcaa agataaggct ttaaatgatc taaggccg 60  
attaaattcc aac 73

<210> 7  
<211> 80  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide

<400> 7  
ccttaggctt ataacatcac attaaaagc atctcagcct accatgagaa taagagaaag 60  
aaaatgaaga tcaaaagctt 80

<210> 8  
<211> 31  
<212> DNA  
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<223> Description of Artificial Sequence: Synthetic  
oligodeoxynucleotide

<400> 8  
gtgtttcgtc gagacgccc caagagttag 9 31

<210> 9  
<211> 34  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: Synthetic  
oligodeoxynucleotide

<400> 9  
ggtgtgtttc gtagatctgc acacaagagt gagg 34

<210> 10  
<211> 38  
<212> DNA  
<213> Artificial Sequence

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<400> 10	ccaggggtgt gttcgtcga aagaaagtgg tgctggc	38
<210> 11		
<211> 33		
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oligodeoxynucleotide		
<400> 11	ccaactctga caccgacgccc acctgcttc agg	33
<210> 12		
<211> 27		
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oligodeoxynucleotide		
<400> 12	gctagcttgc gacgccgggg gaattcg	27
<210> 13		
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<213> Artificial Sequence		
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oligodeoxynucleotide		
<400> 13	gcagaaccag aaggacgcca aggtggagtt c	31
<210> 14		
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<210> 15		
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligodeoxynucleotide

<400> 15
actgccaact ctgacaccta aaagcttgg a tcccacctgc ttcaggggca g      51

<210> 16
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligodeoxynucleotide

<400> 16
ggtaggtcgt gtggacgcca gatctttgg aagaattgcc cgtctggaaag      50

<210> 17
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligodeoxynucleotide

<400> 17
ctgcaggta ggcgtcgcca accagttgct tcagctgtgc      40

<210> 18
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligodeoxynucleotide

<400> 18
gatccccctaa gg      12

<210> 19
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligodeoxynucleotide

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<400> 19	
gtgctgggca aacaaggggta tacag	25
<210> 20	
<211> 21	
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oligodeoxynucleotide	
<400> 20	
ggcttaaagc aagtggtgct g	21
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oligodeoxynucleotide	
<400> 21	
tgctttgccg aggaggtaa ggaagacgct aagggttaagt ctgaagaaga agccttaggc 60	69
ttaaagaaa	
<210> 22	
<211> 50	
<212> DNA	
<213> Artificial Sequence	
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<223> Description of Artificial Sequence: Synthetic	
oligodeoxynucleotide	
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cccggaagc ttcccttaggc ttaaagaaaag tggtgctggg caaaaaagg 50	
<210> 23	
<211> 39	
<212> DNA	
<213> Artificial Sequence	
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oligodeoxynucleotide	
<400> 23	
cccggaagc ttttagaaaag ctagcaccac gatgtctat	39

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<210> 24
<211> 563
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: MstII-SmaI
      restriction fragment including the V1 and V2
      domains of the CD4 receptor of the HIV-1 virus

<400> 24
ccttaggctt aaagaaaagtg gtgctggca aaaaagggga tacagtggaa ctgaccctgta 60
cagttccca gaagaagagc atacaattcc actggaaaaaa ctccaaaccag ataaagattc 120
tgggaaatca gggctccttc ttaactaaag gtccatccaa gctgaatgat cgcgctgact 180
caagaagaag cctttggac caagggaaact tccccctgat catcaagaat cttaagatag 240
aagactcaga tacttacatc tgtgaagtgg aggaccagaa ggaggaggtg caattgctag 300
tgttcggatt gactgccaac tctgacaccc acctgcttca ggggcagagc ctgaccctga 360
ccttggagag cccccctggt agtagccccct cagtgcaatg taggagtcca aggggtaaaa 420
acatacaggg ggggaagacc ctctccgtgt ctcagctgga gctccaggat agtggcacct 480
ggacatgcac tgtcttgcag aaccagaaga aggtggagtt caaaatagac atcgtggtgc 540
tagcttctca aaagcttccc ggg 563

<210> 25
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Restriction
      fragment HindIII coding for the protein fusion
      preproto-HSA-V1V2

<220>
<221> CDS
<222> (7)..(2370)

<400> 25
aagctt atg aag tgg gta acc ttt att tcc ctt ctt ttt ctc ttt agc 48
  Met Lys Trp Val Thr Phe Ile Ser Leu Leu Phe Leu Phe Ser
    1           5           10

tcg gct tat tcc agg ggt gtg ttt cgt cga gat gca cac aag agt gag 96
  Ser Ala Tyr Ser Arg Gly Val Phe Arg Arg Asp Ala His Lys Ser Glu
    15          20          25          30

gtt gct cat cgg ttt aaa gat ttg gga gaa gaa aat ttc aaa gcc ttg 144
  Val Ala His Arg Phe Lys Asp Leu Gly Glu Glu Asn Phe Lys Ala Leu
    35          40          45

gtg ttg att gcc ttt gct cag tat ctt cag cag tgt cca ttt gaa gat 192
  Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln Gln Cys Pro Phe Glu Asp
    50          55          60

cat gta aaa tta gtg aat gaa gta act gaa ttt gca aaa aca tgt gtt 240
  His Val Lys Leu Val Asn Glu Val Thr Glu Phe Ala Lys Thr Cys Val
    65          70          75

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gct gat gag tca gct gaa aat tgt gac aaa tca ctt cat acc ctt ttt Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys Ser Leu His Thr Leu Phe 80 85 90	288
gga gac aaa tta tgc aca gtt gca act ctt cgt gaa acc tat ggt gaa Gly Asp Lys Leu Cys Thr Val Ala Thr Leu Arg Glu Thr Tyr Gly Glu 95 100 105 110	336
atg gct gac tgc tgt gca aaa caa gaa cct gag aga aat gaa tgc ttc Met Ala Asp Cys Cys Ala Lys Gln Glu Pro Glu Arg Asn Glu Cys Phe 115 120 125	384
ttg caa cac aaa gat gac aac cca aac ctc ccc cga ttg gtg aga cca Leu Gln His Lys Asp Asp Asn Pro Asn Leu Pro Arg Leu Val Arg Pro 130 135 140	432
gag gtt gat gtg atg tgc act gct ttt cat gac aat gaa gag aca ttt Glu Val Asp Val Met Cys Thr Ala Phe His Asp Asn Glu Glu Thr Phe 145 150 155	480
ttg aaa aaa tac tta tat gaa att gcc aga aga cat cct tac ttt tat Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg Arg His Pro Tyr Phe Tyr 160 165 170	528
gcc ccg gaa ctc ctt ttc ttt gct aaa agg tat aaa gct gct ttt aca Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg Tyr Lys Ala Ala Phe Thr 175 180 185 190	576
gaa tgt tgc caa gct gct gat aaa gct gcc tgc ctg ttg cca aag ctc Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala Cys Leu Leu Pro Lys Leu 195 200 205	624
gat gaa ctt cgg gat gaa ggg aag gct tcg tct gcc aaa cag aga ctc Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser Ser Ala Lys Gln Arg Leu 210 215 220	672
aag tgt gcc agt ctc caa aaa ttt gga gaa aga gct ttc aaa gca tgg Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu Arg Ala Phe Lys Ala Trp 225 230 235	720
gca gta gct cgc ctg agc cag aga ttt ccc aaa gct gag ttt gca gaa Ala Val Ala Arg Leu Ser Gln Arg Phe Pro Lys Ala Glu Phe Ala Glu 240 245 250	768
gtt tcc aag tta gtg aca gat ctt acc aaa gtc cac acg gaa tgc tgc Val Ser Lys Leu Val Thr Asp Leu Thr Lys Val His Thr Glu Cys Cys 255 260 265 270	816
cat gga gat ctg ctt gaa tgt gct gat gac agg gcg gac ctt gcc aag His Gly Asp Leu Leu Glu Cys Ala Asp Asp Arg Ala Asp Leu Ala Lys 275 280 285	864
tat atc tgt gaa aat caa gat tcg atc tcc agt aaa ctg aag gaa tgc Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser Ser Lys Leu Lys Glu Cys 290 295 300	912

tgt gaa aaa cct ctg ttg gaa aaa tcc cac tgc att gcc gaa gtg gaa	960
Cys Glu Lys Pro Leu Leu Glu Lys Ser His Cys Ile Ala Glu Val Glu	
305 310 315	
aat gat gag atg cct gct gac ttg cct tca tta gct gct gat ttt gtt	1008
Asn Asp Glu Met Pro Ala Asp Leu Pro Ser Leu Ala Ala Asp Phe Val	
320 325 330	
gaa agt aag gat gtt tgc aaa aac tat gct gag gca aag gat gtc ttc	1056
Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala Glu Ala Lys Asp Val Phe	
335 340 345 350	
ctg ggc atg ttt ttg tat gaa tat gca aga agg cat cct gat tac tct	1104
Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg Arg His Pro Asp Tyr Ser	
355 360 365	
gtc gta ctg ctg ctg aga ctt gcc aag aca tat gaa acc act cta gag	1152
Val Val Leu Leu Arg Leu Ala Lys Thr Tyr Glu Thr Thr Leu Glu	
370 375 380	
aag tgc tgt gcc gct gca gat cct cat gaa tat gtc gat gtc aaa gtg ttc	1200
Lys Cys Cys Ala Ala Ala Asp Pro His Glu Cys Tyr Ala Lys Val Phe	
385 390 395	
gat gaa ttt aaa cct ctt gtg gaa gag cct cag aat tta atc aaa caa	1248
Asp Glu Phe Lys Pro Leu Val Glu Glu Pro Gln Asn Leu Ile Lys Gln	
400 405 410	
aat tgt gag ctt ttt gag cag ctt gga gag tac aaa ttc cag aat gcg	1296
Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu Tyr Lys Phe Gln Asn Ala	
415 420 425 430	
cta tta gtt cgt tac acc aag aaa gta ccc caa gtg tca act cca act	1344
Leu Leu Val Arg Tyr Thr Lys Lys Val Pro Gln Val Ser Thr Pro Thr	
435 440 445	
ctt gta gag gtc tca aga aac cta gga aaa gtg ggc aqc aaa tgt tgt	1392
Leu Val Glu Val Ser Arg Asn Leu Gly Lys Val Gly Ser Lys Cys Cys	
450 455 460	
aaa cat cct gaa gca aaa aga atg ccc tgt gca gaa gac tat cta tcc	1440
Lys His Pro Glu Ala Lys Arg Met Pro Cys Ala Glu Asp Tyr Leu Ser	
465 470 475	
gtg gtc ctg aac cag tta tgt gtg ttg cat gag aaa acg cca gta agt	1488
Val Val Leu Asn Gln Leu Cys Val Leu His Glu Lys Thr Pro Val Ser	
480 485 490	
gac aga gtc acc aaa tgc tgc aca gaa tcc ttg gtg aac agg cga cca	1536
Asp Arg Val Thr Lys Cys Cys Thr Glu Ser Leu Val Asn Arg Arg Pro	
495 500 505 510	
tgc ttt tca gct ctg gaa gtc gat gaa aca tac gtt ccc aaa gag ttt	1584
Cys Phe Ser Ala Leu Glu Val Asp Glu Thr Tyr Val Pro Lys Glu Phe	
515 520 525	

aat gct gaa aca ttc acc ttc cat gca gat ata tgc aca ctt tct gag		1632	
Asn Ala Glu Thr Phe Thr Phe His Ala Asp Ile Cys Thr Leu Ser Glu			
530	535	540	
aag gag aga caa atc aag aaa caa act gca ctt gtt gag ctt gtg aaa		1680	
Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala Leu Val Glu Leu Val Lys			
545	550	555	
cac aag ccc aag gca aca aaa gag caa ctg aaa gct gtt atg gat gat		1728	
His Lys Pro Lys Ala Thr Lys Glu Gln Leu Lys Ala Val Met Asp Asp			
560	565	570	
ttc gca gct ttt gta gag aag tgc tgc aag gct gac gat aag gag acc		1776	
Phe Ala Ala Phe Val Glu Lys Cys Cys Lys Ala Asp Asp Lys Glu Thr			
575	580	585	590
tgc ttt gcc gag gag ggt aaa aaa ctt gtt gct gca agt caa gct gcc		1824	
Cys Phe Ala Glu Glu Gly Lys Lys Leu Val Ala Ala Ser Gln Ala Ala			
595	600	605	
tta ggc tta aag aaa gtg gtg ctg ggc aaa aaa ggg gat aca gtg gaa		1872	
Leu Gly Leu Lys Lys Val Val Leu Gly Lys Lys Gly Asp Thr Val Glu			
610	615	620	
ctg acc tgt aca gct tcc cag aag aag agc ata caa ttc cac tgg aaa		1920	
Leu Thr Cys Thr Ala Ser Gln Lys Ser Ile Gln Phe His Trp Lys			
625	630	635	
aac tcc aac cag ata aag att ctg gga aat cag ggc tcc ttc tta act		1968	
Asn Ser Asn Gln Ile Lys Ile Leu Gly Asn Gln Gly Ser Phe Leu Thr			
640	645	650	
aaa ggt cca tcc aag ctg aat gat cgc gct gac tca aga aga agc ctt		2016	
Lys Gly Pro Ser Lys Leu Asn Asp Arg Ala Asp Ser Arg Arg Ser Leu			
655	660	665	670
tgg gac caa gga aac ttc ccc ctg atc atc aag aat ctt aag ata gaa		2064	
Trp Asp Gln Gly Asn Phe Pro Leu Ile Ile Lys Asn Leu Lys Ile Glu			
675	680	685	
gac tca gat act tac atc tgt gaa gtg gag gac cag aag gag gag gtg		2112	
Asp Ser Asp Thr Tyr Ile Cys Glu Val Glu Asp Gln Lys Glu Glu Val			
690	695	700	
caa ttg cta gtg ttc gga ttg act gcc aac tct gac acc cac ctg ctt		2160	
Gln Leu Leu Val Phe Gly Leu Thr Ala Asn Ser Asp Thr His Leu Leu			
705	710	715	
cag ggg cag agc ctg acc ctg acc ttg gag agc ccc cct ggt agt agc		2208	
Gln Gly Gln Ser Leu Thr Leu Thr Leu Glu Ser Pro Pro Gly Ser Ser			
720	725	730	
ccc tca gtg caa tgt agg agt cca agg ggt aaa aac ata cag ggg ggg		2256	
Pro Ser Val Gln Cys Arg Ser Pro Arg Gly Lys Asn Ile Gln Gly Gly			
735	740	745	750

aag acc ctc tcc gtg tct cag ctg gag ctc cag gat agt ggc acc tgg 2304  
 Lys Thr Leu Ser Val Ser Gln Leu Glu Leu Gln Asp Ser Gly Thr Trp  
 755 760 765

aca tgc act gtc ttg cag aac cag aag aag gtg gag ttc aaa ata gac 2352  
 Thr Cys Thr Val Leu Gln Asn Gln Lys Lys Val Glu Phe Lys Ile Asp  
 770 775 780

atc gtg gtg cta gct ttc taaaagctt 2379  
 Ile Val Val Leu Ala Phe  
 785

<210> 26  
 <211> 788  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Protein fusion  
 prepro-HSA-V1V2

<400> 26  
 Met Lys Trp Val Thr Phe Ile Ser Leu Leu Phe Leu Phe Ser Ser Ala  
 1 5 10 15

Tyr Ser Arg Gly Val Phe Arg Arg Asp Ala His Lys Ser Glu Val Ala  
 20 25 30

His Arg Phe Lys Asp Leu Gly Glu Glu Asn Phe Lys Ala Leu Val Leu  
 35 40 45

Ile Ala Phe Ala Gln Tyr Leu Gln Gln Cys Pro Phe Glu Asp His Val  
 50 55 60

Lys Leu Val Asn Glu Val Thr Glu Phe Ala Lys Thr Cys Val Ala Asp  
 65 70 75 80

Glu Ser Ala Glu Asn Cys Asp Lys Ser Leu His Thr Leu Phe Gly Asp  
 85 90 95

Lys Leu Cys Thr Val Ala Thr Leu Arg Glu Thr Tyr Gly Glu Met Ala  
 100 105 110

Asp Cys Cys Ala Lys Gln Glu Pro Glu Arg Asn Glu Cys Phe Leu Gln  
 115 120 125

His Lys Asp Asp Asn Pro Asn Leu Pro Arg Leu Val Arg Pro Glu Val  
 130 135 140

Asp Val Met Cys Thr Ala Phe His Asp Asn Glu Glu Thr Phe Leu Lys  
 145 150 155 160

Lys Tyr Leu Tyr Glu Ile Ala Arg Arg His Pro Tyr Phe Tyr Ala Pro  
 165 170 175

Glu Leu Leu Phe Phe Ala Lys Arg Tyr Lys Ala Ala Phe Thr Glu Cys  
 180 185 190

Cys Gln Ala Ala Asp Lys Ala Ala Cys Leu Leu Pro Lys Leu Asp Glu  
 195 200 205

Leu Arg Asp Glu Gly Lys Ala Ser Ser Ala Lys Gln Arg Leu Lys Cys  
 210 215 220

Ala Ser Leu Gln Lys Phe Gly Glu Arg Ala Phe Lys Ala Trp Ala Val  
 225 230 235 240

Ala Arg Leu Ser Gln Arg Phe Pro Lys Ala Glu Phe Ala Glu Val Ser  
 245 250 255

Lys Leu Val Thr Asp Leu Thr Lys Val His Thr Glu Cys Cys His Gly  
 260 265 270

Asp Leu Leu Glu Cys Ala Asp Asp Arg Ala Asp Leu Ala Lys Tyr Ile  
 275 280 285

Cys Glu Asn Gln Asp Ser Ile Ser Ser Lys Leu Lys Glu Cys Cys Glu  
 290 295 300

Lys Pro Leu Leu Glu Lys Ser His Cys Ile Ala Glu Val Glu Asn Asp  
 305 310 315 320

Glu Met Pro Ala Asp Leu Pro Ser Leu Ala Ala Asp Phe Val Glu Ser  
 325 330 335

Lys Asp Val Cys Lys Asn Tyr Ala Glu Ala Lys Asp Val Phe Leu Gly  
 340 345 350

Met Phe Leu Tyr Glu Tyr Ala Arg Arg His Pro Asp Tyr Ser Val Val  
 355 360 365

Leu Leu Leu Arg Leu Ala Lys Thr Tyr Glu Thr Thr Leu Glu Lys Cys  
 370 375 380

Cys Ala Ala Ala Asp Pro His Glu Cys Tyr Ala Lys Val Phe Asp Glu  
 385 390 395 400

Phe Lys Pro Leu Val Glu Glu Pro Gln Asn Leu Ile Lys Gln Asn Cys  
 405 410 415

Glu Leu Phe Glu Gln Leu Gly Glu Tyr Lys Phe Gln Asn Ala Leu Leu  
 420 425 430

Val Arg Tyr Thr Lys Lys Val Pro Gln Val Ser Thr Pro Thr Leu Val  
 435 440 445

Glu Val Ser Arg Asn Leu Gly Lys Val Gly Ser Lys Cys Cys Lys His  
 450 455 460

Pro Glu Ala Lys Arg Met Pro Cys Ala Glu Asp Tyr Leu Ser Val Val  
 465 470 475 480

Leu Asn Gln Leu Cys Val Leu His Glu Lys Thr Pro Val Ser Asp Arg  
 485 490 495

B

Val Thr Lys Cys Cys Thr Glu Ser Leu Val Asn Arg Arg Pro Cys Phe  
 500 505 510

Ser Ala Leu Glu Val Asp Glu Thr Tyr Val Pro Lys Glu Phe Asn Ala  
 515 520 525

Glu Thr Phe Thr Phe His Ala Asp Ile Cys Thr Leu Ser Glu Lys Glu  
 530 535 540

Arg Gln Ile Lys Lys Gln Thr Ala Leu Val Glu Leu Val Lys His Lys  
 545 550 555 560

Pro Lys Ala Thr Lys Glu Gln Leu Lys Ala Val Met Asp Asp Phe Ala  
 565 570 575

Ala Phe Val Glu Lys Cys Cys Lys Ala Asp Asp Lys Glu Thr Cys Phe  
 580 585 590

Ala Glu Glu Gly Lys Lys Leu Val Ala Ala Ser Gln Ala Ala Leu Gly  
 595 600 605

Leu Lys Lys Val Val Leu Gly Lys Lys Gly Asp Thr Val Glu Leu Thr  
 610 615 620

Cys Thr Ala Ser Gln Lys Lys Ser Ile Gln Phe His Trp Lys Asn Ser  
 625 630 635 640

Asn Gln Ile Lys Ile Leu Gly Asn Gln Gly Ser Phe Leu Thr Lys Gly  
 645 650 655

Pro Ser Lys Leu Asn Asp Arg Ala Asp Ser Arg Arg Ser Leu Trp Asp  
 660 665 670

Gln Gly Asn Phe Pro Leu Ile Ile Lys Asn Leu Lys Ile Glu Asp Ser  
 675 680 685

Asp Thr Tyr Ile Cys Glu Val Glu Asp Gln Lys Glu Glu Val Gln Leu  
 690 695 700

Leu Val Phe Gly Leu Thr Ala Asn Ser Asp Thr His Leu Leu Gln Gly  
 705 710 715 720

Gln Ser Leu Thr Leu Thr Leu Glu Ser Pro Pro Gly Ser Ser Pro Ser  
 725 730 735

Val Gln Cys Arg Ser Pro Arg Gly Lys Asn Ile Gln Gly Gly Lys Thr  
 740 745 750

Leu Ser Val Ser Gln Leu Glu Leu Gln Asp Ser Gly Thr Trp Thr Cys  
 755 760 765

Thr Val Leu Gln Asn Gln Lys Lys Val Glu Phe Lys Ile Asp Ile Val  
 770 775 780

Val Leu Ala Phe  
 785

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<210> 27
<211> 132
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Leucine zipper
      of c-jun in a hybrid nucleotide HSA-CD4

<220>
<221> CDS
<222> (1)..(132)

<400> 27
      aga tct ttg gaa aga att gcc cgt ctg gaa gaa aaa gtg aaa act ctg      48
      Arg Ser Leu Glu Arg Ile Ala Arg Leu Glu Glu Lys Val Lys Thr Leu
      1           5           10          15

      aaa gcc cag aac tct gag ctc gca tcc acg gcc aac atg ctg cgt gaa      96
      Lys Ala Gln Asn Ser Glu Leu Ala Ser Thr Ala Asn Met Leu Arg Glu
      20          25          30

      cag gtt gca cag ctg aag caa ctg gtt ggc gac gcc      132
      Gln Val Ala Gln Leu Lys Gln Leu Val Gly Asp Ala
      35          40

<210> 28
<211> 44
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Leucine zipper
      of c-jun in a hybrid protein HSA-CD4

<400> 28
      Arg Ser Leu Glu Arg Ile Ala Arg Leu Glu Glu Lys Val Lys Thr Leu      15
      1           5           10          15

      Lys Ala Gln Asn Ser Glu Leu Ala Ser Thr Ala Asn Met Leu Arg Glu
      20          25          30

      Gln Val Ala Gln Leu Lys Gln Leu Val Gly Asp Ala
      35          40

<210> 29
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

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<220>
<221> CDS
<222> (1)..(36)

<400> 29
tgc ttt tca gct ctg gaa gtc gat gaa aca tac gtt
Cys Phe Ser Ala Leu Glu Val Asp Glu Thr Tyr Val
1 5 10

36

<210> 30
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 30
Cys Phe Ser Ala Leu Glu Val Asp Glu Thr Tyr Val
1 5 10

<210> 31
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<220>
<221> CDS
<222> (1)..(27)

<400> 31
tca gct ctg gaa gtc gat gcc tta ggn
Ser Ala Leu Glu Val Asp Ala Leu Gly
1 5

27

<210> 32
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 32
Cys Phe Ser Ala Leu Glu Val Asp Ala Leu Gly
1 5 10

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<210> 33  
<211> 35  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic peptide

<400> 33  
Cys Phe Ala Glu Glu Gly Lys Lys Leu Val Ala Ala Ser Gln Ala Ala  
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Leu Gly Leu Lys Lys Val Val Leu Gly Lys Lys Gly Asp Thr Val Glu  
20 25 30

Leu Thr Cys  
35

<210> 34  
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<212> PRT  
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<220>  
<223> Description of Artificial Sequence: Synthetic peptide

<220>  
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<223> Ser, Pro, Thr or Ala

<220>  
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<222> (7)  
<223> Any amino acid

<220>  
<221> MOD\_RES  
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<223> Any amino acid

<400> 34  
Cys Xaa Leu Gly Leu Lys Xaa Val Val Leu Gly Lys Xaa Gly Asp Thr  
1 5 10 15

Val Glu Leu Thr Cys  
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<210> 35  
<211> 32  
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<220>  
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<400> 35  
Cys Phe Ala Glu Glu Gly Lys Glu Asp Ala Lys Gly Lys Ser Glu Glu  
1 5 10 15

Glu Ala Leu Gly Leu Lys Lys Val Val Leu Gly Lys Lys Gly Asp Thr  
20 25 30

<210> 36  
<211> 22  
<212> PRT  
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<220>  
<223> Description of Artificial Sequence: Synthetic peptide

<400> 36  
Arg Gly Val Phe Arg Arg Lys Lys Val Val Leu Gly Lys Lys Gly Asp  
1 5 10 15

Thr Val Glu Leu Thr Cys  
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*B*

<210> 37  
<211> 22  
<212> PRT  
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<220>  
<223> Description of Artificial Sequence: Synthetic peptide

<220>  
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<223> Any amino acid

<220>  
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<400> 37  
Arg Gly Val Phe Arg Arg Lys Xaa Val Val Leu Gly Lys Xaa Gly Asp  
1 5 10 15

Thr Val Glu Leu Thr Cys  
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<210> 38  
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<212> PRT

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<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 38

Cys Glu Val Glu Asp Gln Lys Glu Glu Val Gln Leu Leu Val Phe Gly  
1 5 10 15

Leu Thr Ala Asn Ser Asp Thr Asp Ala His Lys Ser Glu Val  
20 25 30

<210> 39

<211> 28

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 39

Cys Thr Val Leu Gln Asn Gln Lys Lys Val Glu Phe Lys Ile Asp Ile  
1 5 10 15

Val Val Leu Ala Phe Asp Ala His Lys Ser Glu Val  
20 25

<210> 40

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 40

Cys Thr Val Leu Gln Asn Gln Lys Asp Ala His Lys Ser Glu Val  
1 5 10 15

<210> 41

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 41

Cys Asp Ala His Lys Ser Glu Val  
1 5